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## SEQUENCE LISTING

<110> Iwamoto, Aikichi  
Tachikawa, Ai

<120> Methods For Enhancing Exogenous Epitope  
Display on MHC Class 1 Through Inhibition of Tap Activity

<130> 50026/051001

<150> PCT/JP03/12595

<151> 2003-10-01

<150> JP 2002-288394

<151> 2002-10-01

<160> 54

<170> FastSEQ for Windows Version 4.0

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37

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1 5 10

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Leu Leu Ser Leu Ser Gly Leu Glu Ala  
15 20

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<221> CDS  
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Arg Tyr Pro Leu Thr Phe Gly Trp Cys Phe  
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<221> CDS  
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33

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<400> 23  
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<221> CDS  
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48

1	5	10	15	
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act cca aag att 60  
 Thr Pro Lys Ile  
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<210> 25  
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<220>  
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<400> 25  
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 1 5 10 15  
 Thr Pro Lys Ile  
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<210> 26  
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<221> CDS  
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 aag tgg gat cga gac atg taacgtacgc cgtagtaaga aaaacttagg 48  
 Lys Trp Asp Arg Asp Met  
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gtgaaagttc atcgcggccg c 69

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<210> 28  
 <211> 41  
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<220>
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<400> 28
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<210> 29
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caagctgtga g 71

<210> 30
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Met Ala Val Met Ala Pro
1 5

<210> 31
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1 5

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 1 5  
  
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 1 5  
  
  
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 aaat 64  
  
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 <211> 56  
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 <211> 33  
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<212> DNA
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<220>
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<220>
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ttgcgggccgc gatgaacttt caccctaagt ttttcttact acggcgtacg tca      53

<210> 39
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<221> CDS
<222> (44)...(61)

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                                   Met Ser Trp Ala
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ctg gaa      61
Leu Glu
5

<210> 40
<211> 6
<212> PRT
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<220>
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<400> 40
Met Ser Trp Ala Leu Glu
1              5

<210> 41

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<211> 55  
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 <221> CDS  
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 1 5 10  
  
 tgatagcggc cgc 55  
  
 <210> 42  
 <211> 14  
 <212> PRT  
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 <223> Artificially Synthesized Sequence  
  
 <400> 42  
 Arg Asn Pro Val Thr Arg Gly Ala His His His His His His  
 1 5 10  
  
 <210> 43  
 <211> 58  
 <212> DNA  
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 <223> Artificially Synthesized Sequence  
  
 <221> CDS  
 <222> (41)...(58)  
  
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 Met Asp Leu Leu Ile  
 1 5  
  
 cgt 58  
 Arg  
  
 <210> 44  
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<223> Artificially Synthesized Sequence

<400> 44

Met Asp Leu Leu Ile Arg  
1 5

<210> 45

<211> 55

<212> DNA

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<221> CDS

<222> (1)...(42)

<400> 45

att cga cgt tgt ggc tcc gga gct cac cac cat cac cac cat 42  
Ile Arg Arg Cys Gly Ser Gly Ala His His His His His His  
1 5 10

tgatagcggc cgc 55

<210> 46

<211> 14

<212> PRT

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<220>

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<400> 46

Ile Arg Arg Cys Gly Ser Gly Ala His His His His His His  
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<210> 47

<211> 2960

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (165)...(2588)

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tatctagtga gcaggcggcc gctttcgatt togttttccc ctaa atg gct gag ctt 176  
Met Ala Glu Leu  
1

ctc gcc agc gca gga tca gcc tgt tcc tgg gac ttt ccg aga gcc ccg 224  
Leu Ala Ser Ala Gly Ser Ala Cys Ser Trp Asp Phe Pro Arg Ala Pro  
5 10 15 20

ccc tgc ttc cct ccc cca gcc gcc agt agg gga gga ctc ggc ggt acc	272
Pro Ser Phe Pro Pro Pro Ala Ala Ser Arg Gly Gly Leu Gly Gly Thr	
25 30 35	
cgg agc ttc agg ccc cac cgg ggc gcg gag agt ccc agg ccc ggc cgg	320
Arg Ser Phe Arg Pro His Arg Gly Ala Glu Ser Pro Arg Pro Gly Arg	
40 45 50	
gac cgg gac ggc gtc cga gtg cca atg gct agc tct agg tgt ccc gct	368
Asp Arg Asp Gly Val Arg Val Pro Met Ala Ser Ser Arg Cys Pro Ala	
55 60 65	
ccc cgc ggg tgc cgc tgc ctc ccc gga gct tct ctc gca tgg ctg ggg	416
Pro Arg Gly Cys Arg Cys Leu Pro Gly Ala Ser Leu Ala Trp Leu Gly	
70 75 80	
aca gta ctg cta ctt ctc gcc gac tgg gtg ctg ctc cgg acc gcg ctg	464
Thr Val Leu Leu Leu Leu Ala Asp Trp Val Leu Leu Arg Thr Ala Leu	
85 90 95 100	
ccc cgc ata ttc tcc ctg ctg gtg ccc acc gcg ctg cca ctg ctc cgg	512
Pro Arg Ile Phe Ser Leu Leu Val Pro Thr Ala Leu Pro Leu Leu Arg	
105 110 115	
gtc tgg gcg gtg ggc ctg agc cgc tgg gcc gtg ctc tgg ctg ggg gcc	560
Val Trp Ala Val Gly Leu Ser Arg Trp Ala Val Leu Trp Leu Gly Ala	
120 125 130	
tgc ggg gtc ctc agg gca acg gtt ggc tcc aag agc gaa aac gca ggt	608
Cys Gly Val Leu Arg Ala Thr Val Gly Ser Lys Ser Glu Asn Ala Gly	
135 140 145	
gcc cag ggc tgg ctg gct gct ttg aag cca tta gct gcg gca ctg ggc	656
Ala Gln Gly Trp Leu Ala Ala Leu Lys Pro Leu Ala Ala Ala Leu Gly	
150 155 160	
ttg gcc ctg ccg gga ctt gcc ttg ttc cga gag ctg atc tca tgg gga	704
Leu Ala Leu Pro Gly Leu Ala Leu Phe Arg Glu Leu Ile Ser Trp Gly	
165 170 175 180	
gcc ccc ggg tcc gcg gat agc acc agg cta ctg cac tgg gga agt cac	752
Ala Pro Gly Ser Ala Asp Ser Thr Arg Leu Leu His Trp Gly Ser His	
185 190 195	
cct acc gcc ttc gtt gtc agt tat gca gcg gca ctg ccc gca gca gcc	800
Pro Thr Ala Phe Val Val Ser Tyr Ala Ala Ala Leu Pro Ala Ala Ala	
200 205 210	
ctg tgg cac aaa ctc ggg agc ctc tgg gtg ccc ggc ggt cag ggc ggc	848
Leu Trp His Lys Leu Gly Ser Leu Trp Val Pro Gly Gly Gln Gly Gly	
215 220 225	
tct gga aac cct gtg cgt cgg ctt cta ggc tgc ctg ggc tcg gag acg	896
Ser Gly Asn Pro Val Arg Arg Leu Leu Gly Cys Leu Gly Ser Glu Thr	
230 235 240	

cgc cgc ctc tcg ctg ttc ctg gtc ctg gtg gtc ctc tcc tct ctt ggg	944
Arg Arg Leu Ser Leu Phe Leu Val Leu Val Val Leu Ser Ser Leu Gly	
245 250 255 260	
gag atg gcc att cca ttc ttt acg ggc cgc ctc act gac tgg att cta	992
Glu Met Ala Ile Pro Phe Phe Thr Gly Arg Leu Thr Asp Trp Ile Leu	
265 270 275	
caa gat ggc tca gcc gat acc ttc act cga aac tta act ctc atg tcc	1040
Gln Asp Gly Ser Ala Asp Thr Phe Thr Arg Asn Leu Thr Leu Met Ser	
280 285 290	
att ctc acc ata gcc agt gca gtg ctg gag ttc gtg ggt gac ggg atc	1088
Ile Leu Thr Ile Ala Ser Ala Val Leu Glu Phe Val Gly Asp Gly Ile	
295 300 305	
tat aac aac acc atg ggc cac gtg cac agc cac ttg cag gga gag gtg	1136
Tyr Asn Asn Thr Met Gly His Val His Ser His Leu Gln Gly Glu Val	
310 315 320	
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Phe Gly Ala Val Leu Arg Gln Glu Thr Glu Phe Phe Gln Gln Asn Gln	
325 330 335 340	
aca ggt aac atc atg tct cgg gta aca gag gac acg tcc acc ctg agt	1232
Thr Gly Asn Ile Met Ser Arg Val Thr Glu Asp Thr Ser Thr Leu Ser	
345 350 355	
gat tct ctg agt gag aat ctg agc tta ttt ctg tgg tac ctg gtg cga	1280
Asp Ser Leu Ser Glu Asn Leu Ser Leu Phe Leu Trp Tyr Leu Val Arg	
360 365 370	
ggc cta tgt ctc ttg ggg atc atg ctc tgg gga tca gtg tcc ctc acc	1328
Gly Leu Cys Leu Leu Gly Ile Met Leu Trp Gly Ser Val Ser Leu Thr	
375 380 385	
atg gtc acc ctg atc acc ctg cct ctg ctt ttc ctt ctg ccc aag aag	1376
Met Val Thr Leu Ile Thr Leu Pro Leu Leu Phe Leu Leu Pro Lys Lys	
390 395 400	
gtg gga aaa tgg tac cag ttg ctg gaa gtg cag gtg cgg gaa tct ctg	1424
Val Gly Lys Trp Tyr Gln Leu Leu Glu Val Gln Val Arg Glu Ser Leu	
405 410 415 420	
gca aag tcc agc cag gtg gcc att gag gct ctg tcg gcc atg cct aca	1472
Ala Lys Ser Ser Gln Val Ala Ile Glu Ala Leu Ser Ala Met Pro Thr	
425 430 435	
gtt cga agc ttt gcc aac gag gag ggc gaa gcc cag aag ttt agg gaa	1520
Val Arg Ser Phe Ala Asn Glu Glu Gly Glu Ala Gln Lys Phe Arg Glu	
440 445 450	
aag ctg caa gaa ata aag aca ctc aac cag aag gag gct gtg gcc tat	1568
Lys Leu Gln Glu Ile Lys Thr Leu Asn Gln Lys Glu Ala Val Ala Tyr	
455 460 465	
gca gtc aac tcc tgg acc act agt att tca ggt atg ctg ctg aaa gtg	1616

Ala Val Asn Ser Trp Thr Thr Ser Ile Ser Gly Met Leu Leu Lys Val	
470 475 480	
gga atc ctc tac att ggt ggg cag ctg gtg acc agt ggg gct gta agc	1664
Gly Ile Leu Tyr Ile Gly Gly Gln Leu Val Thr Ser Gly Ala Val Ser	
485 490 495 500	
agt ggg aac ctt gtc aca ttt gtt ctc tac cag atg cag ttc acc cag	1712
Ser Gly Asn Leu Val Thr Phe Val Leu Tyr Gln Met Gln Phe Thr Gln	
505 510 515	
gct gtg gag gta ctg ctc tcc atc tac ccc aga gta cag aag gct gtg	1760
Ala Val Glu Val Leu Leu Ser Ile Tyr Pro Arg Val Gln Lys Ala Val	
520 525 530	
ggc tcc tca gag aaa ata ttt gag tac ctg gac cgc acc cct cgc tgc	1808
Gly Ser Ser Glu Lys Ile Phe Glu Tyr Leu Asp Arg Thr Pro Arg Cys	
535 540 545	
cca ccc agt ggt ctg ttg act ccc tta cac ttg gag ggc ctt gtc cag	1856
Pro Pro Ser Gly Leu Leu Thr Pro Leu His Leu Glu Gly Leu Val Gln	
550 555 560	
ttc caa gat gtc tcc ttt gcc tac cca aac cgc cca gat gtc tta gtg	1904
Phe Gln Asp Val Ser Phe Ala Tyr Pro Asn Arg Pro Asp Val Leu Val	
565 570 575 580	
cta cag ggg ctg aca ttc acc cta cgc cct ggc gag gtg acg gcg ctg	1952
Leu Gln Gly Leu Thr Phe Thr Leu Arg Pro Gly Glu Val Thr Ala Leu	
585 590 595	
gtg gga ccc aat ggg tct ggg aag agc aca gtg gct gcc ctg ctg cag	2000
Val Gly Pro Asn Gly Ser Gly Lys Ser Thr Val Ala Ala Leu Leu Gln	
600 605 610	
aat ctg tac cag ccc acc ggg gga cag ctg ctg ttg gat ggg aag ccc	2048
Asn Leu Tyr Gln Pro Thr Gly Gly Gln Leu Leu Leu Asp Gly Lys Pro	
615 620 625	
ctt ccc caa tat gag cac cgc tac ctg cac agg cag gtg gct gca gtg	2096
Leu Pro Gln Tyr Glu His Arg Tyr Leu His Arg Gln Val Ala Ala Val	
630 635 640	
gga caa gag cca cag gta ttt gga aga agt ctt caa gaa aat att gcc	2144
Gly Gln Glu Pro Gln Val Phe Gly Arg Ser Leu Gln Glu Asn Ile Ala	
645 650 655 660	
tat ggc ctg acc cag aag cca act atg gag gaa atc aca gct gct gca	2192
Tyr Gly Leu Thr Gln Lys Pro Thr Met Glu Glu Ile Thr Ala Ala Ala	
665 670 675	
gta aag tct ggg gcc cat agt ttc atc tct gga ctc cct cag ggc tat	2240
Val Lys Ser Gly Ala His Ser Phe Ile Ser Gly Leu Pro Gln Gly Tyr	
680 685 690	
gac aca gag gta gac gag gct ggg agc cag ctg tca ggg ggt cag cga	2288
Asp Thr Glu Val Asp Glu Ala Gly Ser Gln Leu Ser Gly Gly Gln Arg	

695	700	705	
cag gca gtg gcg ttg gcc cga gca ttg atc cgg aaa ccg tgt gta ctt			2336
Gln Ala Val Ala Leu Ala Arg Ala Leu Ile Arg Lys Pro Cys Val Leu			
710	715	720	
atc ctg gat gat gcc acc agt gcc ctg gat gca aac agc cag tta cag			2384
Ile Leu Asp Asp Ala Thr Ser Ala Leu Asp Ala Asn Ser Gln Leu Gln			
725	730	735	740
gtg gag cag ctc ctg tac gaa agc cct gag cgg tac tcc cgc tca gtg			2432
Val Glu Gln Leu Leu Tyr Glu Ser Pro Glu Arg Tyr Ser Arg Ser Val			
	745	750	755
ctt ctc atc acc cag cac ctc agc ctg gtg gag cag gct gac cac atc			2480
Leu Leu Ile Thr Gln His Leu Ser Leu Val Glu Gln Ala Asp His Ile			
	760	765	770
ctc ttt ctg gaa gga ggc gct atc cgg gag ggg gga acc cac cag cag			2528
Leu Phe Leu Glu Gly Gly Ala Ile Arg Glu Gly Gly Thr His Gln Gln			
	775	780	785
ctc atg gag aaa aag ggg tgc tac tgg gcc atg gtg cag gct cct gca			2576
Leu Met Glu Lys Lys Gly Cys Tyr Trp Ala Met Val Gln Ala Pro Ala			
	790	795	800
gat gct cca gaa tgaaagcctt ctcagacctg cgcactccat ctccctccct			2628
Asp Ala Pro Glu			
805			
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35 40 45			
Arg Pro Gly Arg Asp Arg Asp Gly Val Arg Val Pro Met Ala Ser Ser			
50 55 60			
Arg Cys Pro Ala Pro Arg Gly Cys Arg Cys Leu Pro Gly Ala Ser Leu			
65 70 75 80			
Ala Trp Leu Gly Thr Val Leu Leu Leu Leu Ala Asp Trp Val Leu Leu			
85 90 95			
Arg Thr Ala Leu Pro Arg Ile Phe Ser Leu Leu Val Pro Thr Ala Leu			
100 105 110			



Pro Leu Leu Arg Val Trp Ala Val Gly Leu Ser Arg Trp Ala Val Leu  
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 Trp Leu Gly Ala Cys Gly Val Leu Arg Ala Thr Val Gly Ser Lys Ser  
 130 135 140  
 Glu Asn Ala Gly Ala Gln Gly Trp Leu Ala Ala Leu Lys Pro Leu Ala  
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 Ala Ala Leu Gly Leu Ala Leu Pro Gly Leu Ala Leu Phe Arg Glu Leu  
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 Ile Ser Trp Gly Ala Pro Gly Ser Ala Asp Ser Thr Arg Leu Leu His  
 180 185 190  
 Trp Gly Ser His Pro Thr Ala Phe Val Val Ser Tyr Ala Ala Ala Leu  
 195 200 205  
 Pro Ala Ala Ala Leu Trp His Lys Leu Gly Ser Leu Trp Val Pro Gly  
 210 215 220  
 Gly Gln Gly Gly Ser Gly Asn Pro Val Arg Arg Leu Leu Gly Cys Leu  
 225 230 235 240  
 Gly Ser Glu Thr Arg Arg Leu Ser Leu Phe Leu Val Leu Val Val Leu  
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 Ser Ser Leu Gly Glu Met Ala Ile Pro Phe Phe Thr Gly Arg Leu Thr  
 260 265 270  
 Asp Trp Ile Leu Gln Asp Gly Ser Ala Asp Thr Phe Thr Arg Asn Leu  
 275 280 285  
 Thr Leu Met Ser Ile Leu Thr Ile Ala Ser Ala Val Leu Glu Phe Val  
 290 295 300  
 Gly Asp Gly Ile Tyr Asn Asn Thr Met Gly His Val His Ser His Leu  
 305 310 315 320  
 Gln Gly Glu Val Phe Gly Ala Val Leu Arg Gln Glu Thr Glu Phe Phe  
 325 330 335  
 Gln Gln Asn Gln Thr Gly Asn Ile Met Ser Arg Val Thr Glu Asp Thr  
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 Ser Thr Leu Ser Asp Ser Leu Ser Glu Asn Leu Ser Leu Phe Leu Trp  
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 Tyr Leu Val Arg Gly Leu Cys Leu Leu Gly Ile Met Leu Trp Gly Ser  
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 Val Ser Leu Thr Met Val Thr Leu Ile Thr Leu Pro Leu Leu Phe Leu  
 385 390 395 400  
 Leu Pro Lys Lys Val Gly Lys Trp Tyr Gln Leu Leu Glu Val Gln Val  
 405 410 415  
 Arg Glu Ser Leu Ala Lys Ser Ser Gln Val Ala Ile Glu Ala Leu Ser  
 420 425 430  
 Ala Met Pro Thr Val Arg Ser Phe Ala Asn Glu Glu Gly Glu Ala Gln  
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 Lys Phe Arg Glu Lys Leu Gln Glu Ile Lys Thr Leu Asn Gln Lys Glu  
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 Ala Val Ala Tyr Ala Val Asn Ser Trp Thr Thr Ser Ile Ser Gly Met  
 465 470 475 480  
 Leu Leu Lys Val Gly Ile Leu Tyr Ile Gly Gly Gln Leu Val Thr Ser  
 485 490 495  
 Gly Ala Val Ser Ser Gly Asn Leu Val Thr Phe Val Leu Tyr Gln Met  
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 530 535 540  
 Thr Pro Arg Cys Pro Pro Ser Gly Leu Leu Thr Pro Leu His Leu Glu  
 545 550 555 560  
 Gly Leu Val Gln Phe Gln Asp Val Ser Phe Ala Tyr Pro Asn Arg Pro



Trp	Leu	Glu	Gly	Thr	Leu	Arg	Leu	Gly	Gly	Leu	Trp	Gly	Leu	Leu	Lys	
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cta	aga	ggg	ctg	ctg	gga	ttt	gtg	ggg	aca	ctg	ctg	ctc	ccg	ctc	tgt	306
Leu	Arg	Gly	Leu	Leu	Gly	Phe	Val	Gly	Thr	Leu	Leu	Leu	Pro	Leu	Cys	
55					60					65					70	
ctg	gcc	acc	ccc	ctg	act	gtc	tcc	ctg	aga	gcc	ctg	gtc	gcg	ggg	gcc	354
Leu	Ala	Thr	Pro	Leu	Thr	Val	Ser	Leu	Arg	Ala	Leu	Val	Ala	Gly	Ala	
				75					80					85		
tca	cgt	gct	ccc	cca	gcc	aga	gtc	gct	tca	gcc	cct	tgg	agc	tgg	ctg	402
Ser	Arg	Ala	Pro	Pro	Ala	Arg	Val	Ala	Ser	Ala	Pro	Trp	Ser	Trp	Leu	
			90					95					100			
ctg	gtg	ggg	tac	ggg	gct	gcg	ggg	ctc	agc	tgg	tca	ctg	tgg	gct	gtt	450
Leu	Val	Gly	Tyr	Gly	Ala	Ala	Gly	Leu	Ser	Trp	Ser	Leu	Trp	Ala	Val	
	105						110					115				
ctg	agc	cct	cct	gga	gcc	cag	gag	aag	gag	cag	gac	cag	gtg	aac	aac	498
Leu	Ser	Pro	Pro	Gly	Ala	Gln	Glu	Lys	Glu	Gln	Asp	Gln	Val	Asn	Asn	
	120					125					130					
aaa	gtc	ttg	atg	tgg	agg	ctg	ctg	aag	ctc	tcc	agg	ccg	gac	ctg	cct	546
Lys	Val	Leu	Met	Trp	Arg	Leu	Leu	Lys	Leu	Ser	Arg	Pro	Asp	Leu	Pro	
135					140					145					150	
ctc	ctc	gtt	gcc	gcc	ttc	ttc	ttc	ctt	gtc	ctt	gct	gtt	ttg	ggt	gag	594
Leu	Leu	Val	Ala	Ala	Phe	Phe	Phe	Leu	Val	Leu	Ala	Val	Leu	Gly	Glu	
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aca	tta	atc	cct	cac	tat	tct	ggt	cgt	gtg	att	gac	atc	ctg	gga	ggt	642
Thr	Leu	Ile	Pro	His	Tyr	Ser	Gly	Arg	Val	Ile	Asp	Ile	Leu	Gly	Gly	
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gat	ttt	gac	ccc	cat	gcc	ttt	gcc	agt	gcc	atc	ttc	ttc	atg	tgc	ctc	690
Asp	Phe	Asp	Pro	His	Ala	Phe	Ala	Ser	Ala	Ile	Phe	Phe	Met	Cys	Leu	
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Phe	Ser	Phe	Gly	Ser	Ser	Leu	Ser	Ala	Gly	Cys	Arg	Gly	Gly	Cys	Phe	
	200					205					210					
acc	tac	acc	atg	tct	cga	atc	aac	ttg	cgg	atc	cgg	gag	cag	ctt	ttc	786
Thr	Tyr	Thr	Met	Ser	Arg	Ile	Asn	Leu	Arg	Ile	Arg	Glu	Gln	Leu	Phe	
215					220					225					230	
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Ser	Ser	Leu	Leu	Arg	Gln	Asp	Leu	Gly	Phe	Phe	Gln	Glu	Thr	Lys	Thr	
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ggg	gag	ctg	aac	tca	cgg	ctg	agc	tcg	gat	acc	acc	ctg	atg	agt	aac	882
Gly	Glu	Leu	Asn	Ser	Arg	Leu	Ser	Ser	Asp	Thr	Thr	Leu	Met	Ser	Asn	
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Trp	Leu	Pro	Leu	Asn	Ala	Asn	Val	Leu	Leu	Arg	Ser	Leu	Val	Lys	Val	

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gtg ggg ctg tat ggc ttc atg ctc agc ata tcg cct cga ctc acc ctc			978
Val Gly Leu Tyr Gly Phe Met Leu Ser Ile Ser Pro Arg Leu Thr Leu			
280	285	290	
ctt tct ctg ctg cac atg ccc ttc aca ata gca gcg gag aag gtg tac			1026
Leu Ser Leu Leu His Met Pro Phe Thr Ile Ala Ala Glu Lys Val Tyr			
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aac acc cgc cat cag gaa gtg ctt cgg gag atc cag gat gca gtg gcc			1074
Asn Thr Arg His Gln Glu Val Leu Arg Glu Ile Gln Asp Ala Val Ala			
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agg gcg ggg cag gtg gtg cgg gaa gcc gtt gga ggg ctg cag acc gtt			1122
Arg Ala Gly Gln Val Val Arg Glu Ala Val Gly Gly Leu Gln Thr Val			
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cgc agt ttt ggg gcc gag gag cat gaa gtc tgt cgc tat aaa gag gcc			1170
Arg Ser Phe Gly Ala Glu Glu His Glu Val Cys Arg Tyr Lys Glu Ala			
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ctt gaa caa tgt cgg cag ctg tat tgg cgg aga gac ctg gaa cgc gcc			1218
Leu Glu Gln Cys Arg Gln Leu Tyr Trp Arg Arg Asp Leu Glu Arg Ala			
	360	365	370
ttg tac ctg ctc ata agg agg gtg ctg cac ttg ggg gtg cag atg ctg			1266
Leu Tyr Leu Leu Ile Arg Arg Val Leu His Leu Gly Val Gln Met Leu			
375	380	385	390
atg ctg agc tgt ggg ctg cag cag atg cag gat ggg gag ctc acc cag			1314
Met Leu Ser Cys Gly Leu Gln Gln Met Gln Asp Gly Glu Leu Thr Gln			
	395	400	405
ggc agc ctg ctt tcc ttt atg atc tac cag gag agc gtg ggg agc tat			1362
Gly Ser Leu Leu Ser Phe Met Ile Tyr Gln Glu Ser Val Gly Ser Tyr			
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Val Gln Thr Leu Val Tyr Ile Tyr Gly Asp Met Leu Ser Asn Val Gly			
	425	430	435
gct gca gag aag gtt ttc tcc tac atg gac cga cag cca aat ctg cct			1458
Ala Ala Glu Lys Val Phe Ser Tyr Met Asp Arg Gln Pro Asn Leu Pro			
	440	445	450
tca cct ggc acg ctt gcc ccc acc act ctg cag ggg gtt gtg aaa ttc			1506
Ser Pro Gly Thr Leu Ala Pro Thr Thr Leu Gln Gly Val Val Lys Phe			
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caa gac gtc tcc ttt gca tat ccc aat cgc cct gac agg cct gtg ctc			1554
Gln Asp Val Ser Phe Ala Tyr Pro Asn Arg Pro Asp Arg Pro Val Leu			
	475	480	485
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Lys Gly Leu Thr Phe Thr Leu Arg Pro Gly Glu Val Thr Ala Leu Val			
	490	495	500

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Gly Pro Asn Gly Ser Gly Lys Ser Thr Val Ala Ala Leu Leu Gln Asn	
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Leu Tyr Gln Pro Thr Gly Gly Gln Val Leu Leu Asp Glu Lys Pro Ile	
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Ser Gln Tyr Glu His Cys Tyr Leu His Ser Gln Val Val Ser Val Gly	
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Gln Glu Pro Val Leu Phe Ser Gly Ser Val Arg Asn Asn Ile Ala Tyr	
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Gly Leu Gln Ser Cys Glu Asp Asp Lys Val Met Ala Ala Ala Gln Ala	
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Ala His Ala Asp Asp Phe Ile Gln Glu Met Glu His Gly Ile Tyr Thr	
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Asp Val Gly Glu Lys Gly Ser Gln Leu Ala Ala Gly Gln Lys Gln Arg	
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Leu Ala Ile Ala Arg Ala Leu Val Arg Asp Pro Arg Val Leu Ile Leu	
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Asp Glu Ala Thr Ser Ala Leu Asp Val Gln Cys Glu Gln Ala Leu Gln	
635 640 645	
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Arg Leu Val Gln Gln Arg Leu Met Asp	
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 <212> PRT  
 <213> Homo sapiens

<400> 50

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Gln	Gly	Leu	Pro	Gly	Leu	Trp	Leu	Glu	Gly	Thr	Leu	Arg	Leu	Gly	Gly
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Leu	Trp	Gly	Leu	Leu	Lys	Leu	Arg	Gly	Leu	Leu	Gly	Phe	Val	Gly	Thr
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Leu	Leu	Leu	Pro	Leu	Cys	Leu	Ala	Thr	Pro	Leu	Thr	Val	Ser	Leu	Arg
65					70					75				80	
Ala	Leu	Val	Ala	Gly	Ala	Ser	Arg	Ala	Pro	Pro	Ala	Arg	Val	Ala	Ser
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Ala	Pro	Trp	Ser	Trp	Leu	Leu	Val	Gly	Tyr	Gly	Ala	Ala	Gly	Leu	Ser
			100					105						110	
Trp	Ser	Leu	Trp	Ala	Val	Leu	Ser	Pro	Pro	Gly	Ala	Gln	Glu	Lys	Glu
	115					120						125			
Gln	Asp	Gln	Val	Asn	Asn	Lys	Val	Leu	Met	Trp	Arg	Leu	Leu	Lys	Leu
	130					135					140				
Ser	Arg	Pro	Asp	Leu	Pro	Leu	Leu	Val	Ala	Ala	Phe	Phe	Phe	Leu	Val
145					150					155				160	
Leu	Ala	Val	Leu	Gly	Glu	Thr	Leu	Ile	Pro	His	Tyr	Ser	Gly	Arg	Val
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Ile	Asp	Ile	Leu	Gly	Gly	Asp	Phe	Asp	Pro	His	Ala	Phe	Ala	Ser	Ala
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Ile	Phe	Phe	Met	Cys	Leu	Phe	Ser	Phe	Gly	Ser	Ser	Leu	Ser	Ala	Gly
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Cys	Arg	Gly	Gly	Cys	Phe	Thr	Tyr	Thr	Met	Ser	Arg	Ile	Asn	Leu	Arg
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Ile	Arg	Glu	Gln	Leu	Phe	Ser	Ser	Leu	Leu	Arg	Gln	Asp	Leu	Gly	Phe

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Phe	Gln	Glu	Thr	Lys	Thr	Gly	Glu	Leu	Asn	Ser	Arg	Leu	Ser	Ser Asp
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Thr	Thr	Leu	Met	Ser	Asn	Trp	Leu	Pro	Leu	Asn	Ala	Asn	Val	Leu Leu
			260					265					270	
Arg	Ser	Leu	Val	Lys	Val	Val	Gly	Leu	Tyr	Gly	Phe	Met	Leu	Ser Ile
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Ser	Pro	Arg	Leu	Thr	Leu	Leu	Ser	Leu	Leu	His	Met	Pro	Phe	Thr Ile
	290					295					300			
Ala	Ala	Glu	Lys	Val	Tyr	Asn	Thr	Arg	His	Gln	Glu	Val	Leu	Arg Glu
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Ile	Gln	Asp	Ala	Val	Ala	Arg	Ala	Gly	Gln	Val	Val	Arg	Glu	Ala Val
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Gly	Gly	Leu	Gln	Thr	Val	Arg	Ser	Phe	Gly	Ala	Glu	Glu	His	Glu Val
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Cys	Arg	Tyr	Lys	Glu	Ala	Leu	Glu	Gln	Cys	Arg	Gln	Leu	Tyr	Trp Arg
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Arg	Asp	Leu	Glu	Arg	Ala	Leu	Tyr	Leu	Leu	Ile	Arg	Arg	Val	Leu His
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Leu	Gly	Val	Gln	Met	Leu	Met	Leu	Ser	Cys	Gly	Leu	Gln	Gln	Met Gln
385			390						395					400
Asp	Gly	Glu	Leu	Thr	Gln	Gly	Ser	Leu	Leu	Ser	Phe	Met	Ile	Tyr Gln
			405					410					415	
Glu	Ser	Val	Gly	Ser	Tyr	Val	Gln	Thr	Leu	Val	Tyr	Ile	Tyr	Gly Asp
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Met	Leu	Ser	Asn	Val	Gly	Ala	Ala	Glu	Lys	Val	Phe	Ser	Tyr	Met Asp
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Arg	Gln	Pro	Asn	Leu	Pro	Ser	Pro	Gly	Thr	Leu	Ala	Pro	Thr	Thr Leu
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Gln	Gly	Val	Val	Lys	Phe	Gln	Asp	Val	Ser	Phe	Ala	Tyr	Pro	Asn Arg
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Pro	Asp	Arg	Pro	Val	Leu	Lys	Gly	Leu	Thr	Phe	Thr	Leu	Arg	Pro Gly
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Glu	Val	Thr	Ala	Leu	Val	Gly	Pro	Asn	Gly	Ser	Gly	Lys	Ser	Thr Val
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Ala	Ala	Leu	Leu	Gln	Asn	Leu	Tyr	Gln	Pro	Thr	Gly	Gly	Gln	Val Leu
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Leu	Asp	Glu	Lys	Pro	Ile	Ser	Gln	Tyr	Glu	His	Cys	Tyr	Leu	His Ser
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Gln	Val	Val	Ser	Val	Gly	Gln	Glu	Pro	Val	Leu	Phe	Ser	Gly	Ser Val
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Arg	Asn	Asn	Ile	Ala	Tyr	Gly	Leu	Gln	Ser	Cys	Glu	Asp	Asp	Lys Val
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Met	Ala	Ala	Ala	Gln	Ala	Ala	His	Ala	Asp	Asp	Phe	Ile	Gln	Glu Met
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Glu	His	Gly	Ile	Tyr	Thr	Asp	Val	Gly	Glu	Lys	Gly	Ser	Gln	Leu Ala
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	610					615				620				
Pro	Arg	Val	Leu	Ile	Leu	Asp	Glu	Ala	Thr	Ser	Ala	Leu	Asp	Val Gln
625				630					635					640
Cys	Glu	Gln	Ala	Leu	Gln	Asp	Trp	Asn	Ser	Arg	Gly	Asp	Arg	Thr Val
			645					650					655	
Leu	Val	Ile	Ala	His	Arg	Leu	Gln	Ala	Val	Gln	Arg	Ala	His	Gln Ile
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Leu	Val	Leu	Gln	Glu	Gly	Lys	Leu	Gln	Lys	Leu	Ala	Gln	Leu	Gln Glu
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Val Gly Pro Arg Thr Tyr Ala Asp Val Arg Asp Glu Ile Asn Lys Arg  
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ggg cgt gag gac cgg gag gcg gcc aga acc gcc gtg cac gac ccg gag 144  
Gly Arg Glu Asp Arg Glu Ala Ala Arg Thr Ala Val His Asp Pro Glu  
35 40 45  
cgt ccc ctg ctg cgc tct ccc ggg ctg ctg ccc gaa atc gcc ccc aac 192  
Arg Pro Leu Leu Arg Ser Pro Gly Leu Leu Pro Glu Ile Ala Pro Asn  
50 55 60  
gca tcc ttg ggt gtg gca cat cga aga acc ggc ggg acc gtg acc gac 240  
Ala Ser Leu Gly Val Ala His Arg Arg Thr Gly Gly Thr Val Thr Asp  
65 70 75 80  
agt ccc cgt aat ccg gta acc cgt 264  
Ser Pro Arg Asn Pro Val Thr Arg  
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<210> 52  
<211> 88  
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<213> Human herpesvirus 1

<400> 52  
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1 5 10 15  
Val Gly Pro Arg Thr Tyr Ala Asp Val Arg Asp Glu Ile Asn Lys Arg  
20 25 30  
Gly Arg Glu Asp Arg Glu Ala Ala Arg Thr Ala Val His Asp Pro Glu  
35 40 45  
Arg Pro Leu Leu Arg Ser Pro Gly Leu Leu Pro Glu Ile Ala Pro Asn  
50 55 60  
Ala Ser Leu Gly Val Ala His Arg Arg Thr Gly Gly Thr Val Thr Asp  
65 70 75 80  
Ser Pro Arg Asn Pro Val Thr Arg  
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<210> 53  
 <211> 549  
 <212> DNA  
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<220>  
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<400> 53  
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 1 5 10 15

acc ccc ggt gag cgg tct tcg cgt gac ccg aaa acc ctt ctc tct ctg 96  
 Thr Pro Gly Glu Arg Ser Ser Arg Asp Pro Lys Thr Leu Leu Ser Leu  
 20 25 30

tct ccg cga caa caa gct tgt gtt ccg aga acg aag tcg cac aga ccc 144  
 Ser Pro Arg Gln Gln Ala Cys Val Pro Arg Thr Lys Ser His Arg Pro  
 35 40 45

gtt tgt tac aac gat aca ggg gac tgc aca gat gca gat gat agc tgg 192  
 Val Cys Tyr Asn Asp Thr Gly Asp Cys Thr Asp Ala Asp Asp Ser Trp  
 50 55 60

aaa cag ctg ggt gag gac ttt gcg cac caa tgc ttg cag gcg gcg aaa 240  
 Lys Gln Leu Gly Glu Asp Phe Ala His Gln Cys Leu Gln Ala Ala Lys  
 65 70 75 80

aag agg cct aaa acg cac aaa tcc cgt ccg aac gat agg aac ctt gag 288  
 Lys Arg Pro Lys Thr His Lys Ser Arg Pro Asn Asp Arg Asn Leu Glu  
 85 90 95

ggg agg ctg acc tgt caa cga gtc cgt ccg cta ctg ccc tgt gat ttg 336  
 Gly Arg Leu Thr Cys Gln Arg Val Arg Arg Leu Leu Pro Cys Asp Leu  
 100 105 110

gat att cat cct agc cac cgg ttg tta acg ctt atg aat aac tgc gtc 384  
 Asp Ile His Pro Ser His Arg Leu Leu Thr Leu Met Asn Asn Cys Val  
 115 120 125

tgt gac ggg gcc gtt tgg aac gcg ttt cgc ttg ata gaa cga cac gga 432  
 Cys Asp Gly Ala Val Trp Asn Ala Phe Arg Leu Ile Glu Arg His Gly  
 130 135 140

ttc ttc gct gtg act ttg tat tta tgt tgc ggg att act ctg ctg gtt 480  
 Phe Phe Ala Val Thr Leu Tyr Leu Cys Cys Gly Ile Thr Leu Leu Val  
 145 150 155 160

gtt att cta gca ttg ctg tgc agc ata aca tac gaa tcg act gga cgt 528  
 Val Ile Leu Ala Leu Leu Cys Ser Ile Thr Tyr Glu Ser Thr Gly Arg  
 165 170 175

ggg att cga cgt tgt ggc tcc  
 Gly Ile Arg Arg Cys Gly Ser  
 180

549

<210> 54  
 <211> 183  
 <212> PRT  
 <213> Human cytomegalovirus

<400> 54  
 Met Asp Leu Leu Ile Arg Leu Gly Phe Leu Leu Met Cys Ala Leu Pro  
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 Thr Pro Gly Glu Arg Ser Ser Arg Asp Pro Lys Thr Leu Leu Ser Leu  
 20 25 30  
 Ser Pro Arg Gln Gln Ala Cys Val Pro Arg Thr Lys Ser His Arg Pro  
 35 40 45  
 Val Cys Tyr Asn Asp Thr Gly Asp Cys Thr Asp Ala Asp Asp Ser Trp  
 50 55 60  
 Lys Gln Leu Gly Glu Asp Phe Ala His Gln Cys Leu Gln Ala Ala Lys  
 65 70 75 80  
 Lys Arg Pro Lys Thr His Lys Ser Arg Pro Asn Asp Arg Asn Leu Glu  
 85 90 95  
 Gly Arg Leu Thr Cys Gln Arg Val Arg Arg Leu Leu Pro Cys Asp Leu  
 100 105 110  
 Asp Ile His Pro Ser His Arg Leu Leu Thr Leu Met Asn Asn Cys Val  
 115 120 125  
 Cys Asp Gly Ala Val Trp Asn Ala Phe Arg Leu Ile Glu Arg His Gly  
 130 135 140  
 Phe Phe Ala Val Thr Leu Tyr Leu Cys Cys Gly Ile Thr Leu Leu Val  
 145 150 155 160  
 Val Ile Leu Ala Leu Leu Cys Ser Ile Thr Tyr Glu Ser Thr Gly Arg  
 165 170 175  
 Gly Ile Arg Arg Cys Gly Ser  
 180